GreenLab: A New Methodology Towards Plant Functional-Structural Model – Structural Part

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GreenLab: A New Methodology towards Plant Functional-Structural Model — Structural Aspect

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Abstract

GreenLab model is an on-going research program conducted jointly by researchers from France and China since 1998. It is oriented to be a functional-structural model for agronomy/forestry applications. Therefore, while keeping a property of being faithful to botanical knowledge, a new methodology is developed within GreenLab by stressing on simplicity of the model. This paper presents briefly our understanding towards plant functional-structural model, but only a model related to plant structures is given to show some progresses of the GreenLab. For a single stand of plant, GreenLab applies its newly developed "dual-scale automaton" approach to generate stochastic structures of plants. Using graph-based interface, this approach provides users with straightforward means of integrating botanical knowledge, i.e., metamers and growth unit, in construction of topological and morphological structures of plants. On the other hand, for a complex tree or a plantation application, a strategy of substructures is employed in GreenLab model for fast construction of plants and calculation of yields in terms of organs. Simulation results indicate promising benefits in using the new methodology to develop a generic plant model in regard to the structural part.

Keywords: plant growth, modeling, structural, functional, automaton, substructure

1 Introduction

Plants, as a typical bio-system, present a real challenge for scientists from all related fields to understand their developmental mechanisms completely and mathematically. Up to now, significant progresses have been reported on studies of modeling, simulation and visualization of plant growth. However, plant growth modeling is still, and will be remained for a long time, a challenge from both theoretical and application points of view. One of difficulties, we believe, is due to the existing boundaries between structural-based and functional-based studies.

In the first group, studies are stressed on the topological and morphological structures of plants. The significant works relate to the development and applications of L-systems [1-4].

Using formal grammars, L-systems can model growth processes in respect of topology information of plants. Another group of study is more traditional and focusing on the physiological mechanisms of plant development due to environmental factors [5-8]. The pioneer work includes the research group leaded by de Wit in Wageningen University of Netherlands since 1970's [9]. However, for agronomy and forestry applications, an integration of two groups of knowledge is necessary. Attempts are made by researchers in developing so-called "functional-structural" models [10,11]. AMAP model is one of the typical studies towards this goal. While its topological and structural models [12-14] aiming at faithful to botanical knowledge [15,16], physiological mechanisms are added in to produce functionality of plant growth [17,18].

Based on the AMAP model and theoretical guidance of Philippe de Reffye, a new methodology is proposed and developed as so called "GreenLab" model. In the rest of this paper, a brief history about GreenLab is firstly introduced. And then a discussion of a conceptual framework of GreenLab is followed to share our understanding in implementation of a functional-structural model. Within this framework, we present only some modeling works in related to the plant structures. Finally, we summarize the works by discussing some philosophy behind GreenLab.

Table 1 Name source of GreenLab from a Chinese ancient poem and its English translation

《长歌行》	*"Long-song Lay"*
- 汉乐府	- Royal Conservatory Songs
青青园中葵，	*Green are the garden mallows! Soon*
朝露待日晞。	*The morning dews will be a-drying.*
阳春布德泽，	*Though wide the blithe Spring shed his boon,*
万物生光辉。	*A radiant world revivifying.*
作者：佚名	Author(s): unknown. Translator: John A. Turner

2 Brief History of GreenLab Team

GreenLab team was started since 1998 under the support of LIAMA (Sino-French Joint Laboratory in Computer Science, Control and Applied Mathematics). The Chinese name for GreenLab is "青园" (pronunciation of "Qing Yuan" with "Green Garden" as the direct meaning), which is adopted from the beginning characters in a Chinese ancient poem (see Table 1) about two thousand years ago (Western Han Dynasty, 206 B.C. - 8 A.C.). Fig.1 shows a logo[+] for GreenLab.

Fig.1 "GreenLab" Logo[+]

GreenLab team consists of researchers from both France and China. The institutions from Chinese side are Institute of Automation and Institute of Machine Intelligence from Chinese Academy of Sciences (CAS), Chinese Agriculture University

[+] Initially designed by Bao-Gang Hu, and refined and drawn by Zhi-Yi Zhang. The name and logo of "GreenLab" are registered by LIAMA.

(CAU), and Chinese Agriculture Academy of Sciences (CAAS). The French research institutes are CIRAD, INRIA, and Ecole Centrale Paris. The objective of GreenLab team is to study internationally on plant growth modeling, simulation and visualization. Theoretical modeling is a main thrust up to now, and we will present new results in the following sections. We recognize that the present GreenLab model is still in a preliminary stage in forming a systematic framework.

3 Conceptual Framework of GreenLab Methodology

GreenLab is oriented to be a dynamic but discrete process model. It adopts the AMAP discretization scheme [17,19] for plant structural modeling. Using growth cycle (GC) as the temporal index, GreenLab obtains the following advantages over the conventional continuous models which are temporized by days or hours. Firstly, a relationship of "yield vs. growth cycle" presents more invariant property (or lesser plot changing) than that of "yield vs. time". Secondly, this model is more reliable by a cycle-based adjustment of the model from the actual observation data of physiologically-aged organs during a plant growth. On the other hand, GreenLab introduces the notion of metamers [17] into a structural model to represent various forms of internodes with bearing leaves and/or flowers. This strategy simplifies organ representations significantly by a compact form.

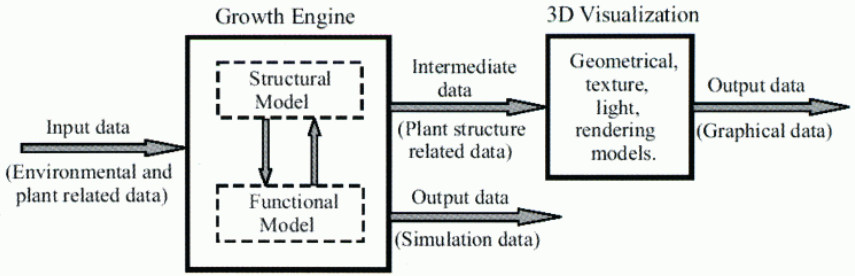

Fig.2 Conceptual framework of GreebLab model

The conceptual framework of GreenLab is illustrated in Fig.2. Basically, GreenLab consists of two modules, namely, "Growth Engine Model" and "3D Visualization Model". Within the Growth Engine Model, we decompose it into two submodels (or models for convenience) for the reason of simplicity. While the structural model is more based on the disciplines of organogenesis or morphogenesis studies, the functional model is more within ecophysiology-based studies. Each model can be further decomposed hierarchically into some specific submodels, say, plant respiration submodel within the functional model.

When simulating a plant growth, there exists a strong degree of coupling effect between structural model and functional model (see data flows in Fig.2). GreenLab proposes a scheme called "Alternating Calculations of Models" in addressing this problem. In this scheme (Fig.3), two models are employed alternatively in simulations. We consider the functional mechanism as an initiative for a plant development. However, within each growth cycle, a structural model is applied first for the calculation, and then is followed by the functional model.

Suppose $\mathcal{F}_i$ and $\mathcal{S}_i$ to be functional-related and structural-related simulation results or states at the ith growth cycle, respectively. Both results can be scalars or sets. For example,

$\mathcal{F}_0$ can be defined as a scalar value of biomass or yield. Usually, one can set $\mathcal{S}_0$ to be zero value or empty set, but $\mathcal{F}_0$ to be known data, say, a biomass of seed. A general form for the alternating calculations of models can be given as

$$\mathcal{S}_i = \psi(\mathcal{S}_{i-1}, \mathcal{F}_{i-1}, \theta_S); \quad i = 1, 2, \cdots \tag{1a}$$

$$\mathcal{F}_i = \varphi(\mathcal{S}_i, \mathcal{F}_{i-1}, \theta_F); \quad i = 1, 2, \cdots \tag{1b}$$

where φ and ψ are functions corresponding to functional and structural models, respectively; and θ is a set of modeling parameters.

However, a systematic study of Eq.(1) is still under investigation for GreenLab. In the following sections, we only show an independent model in regard to plant structural part. It is therefore assumed that a biomass to generate a plant structure is sufficient in this case. The main issue remained is how to describe a plant structure development using a mathematical tool.

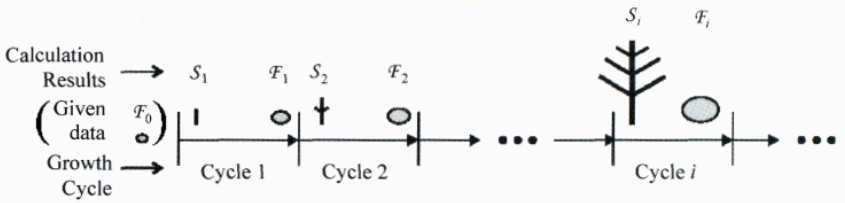

Fig.3 Schematic procedures for alternating calculations of functional model and structural model within GreenLab ($\mathcal{S}_i$ = Results or states from structural calculation at the ith cycle; $\mathcal{F}_i$ = Results or states from functional calculation at the ith cycle)

4 "Dual-Scale Automaton" Approach

In structural model, GreenLab proposes a new approach called "dual-scale automaton" [20] for construction of stochastic structures of plants. This approach follows the same formalism of the conventional automaton theory [21] and stochastic modeling [22], but is restricted within the definitions and construction rules below for plant architecture modeling.

Definition 1: **Macrostate**. A unit that consists of the same set of physiologically-aged entities (or metamers as termed in [17]) in a plant is defined as a macrostate in the automaton. The notation M^i (i=1,2, ...) (see Fig.4) is the ith macrostate for the ith physiologically-aged entities. Each macrostate is represented by a solid ellipse.

Definition 2: **Microstate**. Each type of metamers in a plant is defined as a microstate in the automaton. The notation m^i_r (r=1,2, ...) (see Fig.4) is the rth microstate within the ith macrostate, which corresponds to the rth type of metamer in a plant. Each microstate is represented by a dotted ellipse.

Definition 3: **Structure of dual-scale automaton**. Dual-scale automaton applies two scales (or types) of states, namely, microstate and macrostate, respectively. All macrostates are connected serially, and all microstates are included within the respective macrostate. We call it "Sequential-over-Hierarchical (**SoH**)" structure (Fig.4). It reflects a basic format of the temporal and spatial information to plant structures.

Definition 4: **Transition probability**. Each state can move into another state in a probability manner. p^{ij} is a transition probability from the ith macrostate to the jth macrostate, and p^i_{mn} a transition probability from the mth microstate to the nth microstate within the ith macrostate.

Definition 5: **Normal direction of transition**. We define that a normal direction of the transition in the dual-scale automaton is from left to right, that is, $i \rightarrow (i+j)$ with $j \geq 1$, for both M^i and m^i_r. Otherwise, it is called inverse-normal direction.

Definition 6: **Maximum self-cycling numbers**. Each state is associated with a maximum self-cycling number. When entering the ith state, the process remains there up to this number. After this number is reached in iteration, the current state will make a transition into the jth state according to its associated probability (say, p^{ij}). We denote N^i (i=1, 2, ...) to be a maximum self-cycling number of the ith macrostate, and n^i_r (r=1, 2, ...) to be a maximum self-cycling number for the rth microstate within the ith macrostate.

Definition 7: **Determined plant**. If there is no stochastic process in modeling of a plant, we call it a determined plant. All architectural models defined by botanists [15] can be considered as determined plants. For simplicity, we assume that a determined plant will produce the maximum number of botanical entities. A determined plant presents an up-level estimation of plant yields.

Definition 8: **Database of plants**. Apart from using graph descriptions in Fig.4, dual-scale automaton puts all related data into a database. This database is suggested to be modular-like by including the sub-databases as modulus. The general representation of this database can be defined as

$$\Omega = [\Omega_T \quad \Omega_G \quad \ldots], \tag{2}$$

where Ω_T and Ω_G are sub-databases in related to topological and geometrical parameters, respectively. More sub-databases can be added in for completeness of modeling. Each sub-database can be further organized by another level of sub-databases in relation to their sub-models.

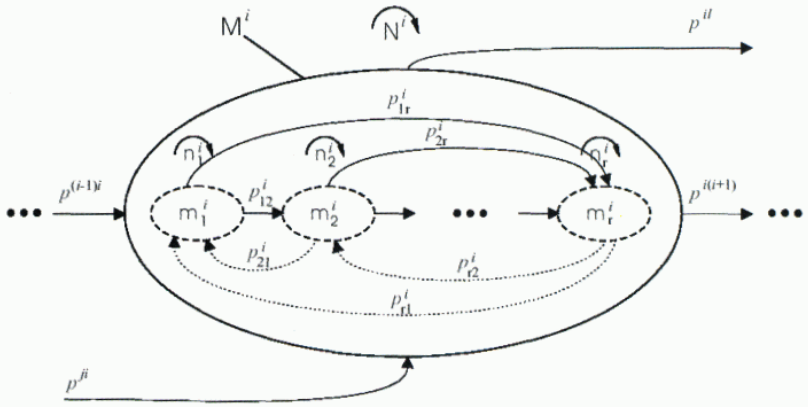

Fig.4 Dual-scale automaton for stochastic process of plant architectures. M^i = the ith macrostate corresponding to a unit having the ith physiological age. m^i_r = the rth microstate inside the ith macrostate for the rth tppe metamer

Construction Rule 1: **Discretization schemes for macrostates**. The temporal discretization for macrostates is growth cycle, defined as the discrete interval of physiological ages of plants [17, 20]. The spatial discretization for macrostates is a growth unit (GU), which usually consists of a series of metamers possessing the same physiological age.

Construction Rule 2: **Discretization schemes for microstates**. The temporal discretization for microstates is an event step in the automaton, which corresponds to a period of generating

a metamer. Therefore, the spatial discretization for microstates is a metamer.

Construction Rule 3: **Construction of macrostates.** Since the macrostates describe botanical units according to their physiological ages, the ordering number of each macrostate should be given to follow the exact age order of physical entity in a real plant. Therefore, the first macrostate, or M^1, always represents for a botanical entity possessing the first physiological age, which is usually the basal part of main axis of a tree. The last macrostate in the automaton is a terminating state of plant axis.

Construction Rule 4: **Construction of microstates.** All metamers having the same physiological age, say, *i*th, should be grouped within the same macrostate, say, m^i_r (r=1,2, …). And, each macrostate should have at least one microstate inside, that is, $r \geq 1$.

Construction Rule 5: **Constraint to self-cycling numbers**. For avoiding the dead-loop in simulation, we impose the use of maximum self-cycling number to each state. This number has to be positive integers and greater or equal to 1 (N^i, $n^i \geq 1$ for any i). This indicates that if a state is entered, it has to be proceeded with at least one time.

Construction Rule 6: **Semi-Markov chains to state transitions**. Dual-scale automaton will form a discrete-time Markov chain. One observes the states of a plant at a discrete set of growth cycles or events as {1, 2, 3, …}. We assume a homogenous property of the transition probabilities. Hence, all p^{ij} and p^i_{mn}, transition probabilities of macrostates and microstates, respectively, are independent of time steps. In addition, due to the visiting times for all states specified by their maximum self-cycling numbers, a semi-Markov chain is suitable to the transitions of both macrostates and microstates, but still satisfies the following properties (the same for p^i_{mn}):

$$0 \leq p^{ij} \leq 1, \tag{3}$$

$$\sum_j p^{ij} = 1, \qquad \text{for any } i. \tag{4}$$

Construction Rule 7: **Constraint to p^{ij}**. All macrostates should transmit in a normal direction. This is required by the irreversible process of plants in respect to the physiological age. That means the branch of physiological age 2 cannot bear the axis of physiological age 1. Therefore, the constraint to p^{ij} is given by

$$p^{ij} = 0, \qquad \text{if } i > j. \tag{5}$$

This constraint indicates an upper triangular matrix for macrostates. For a semi-Markov chain, the diagonal terms of transition matrix are usually set to be zeros ($p^{ii} = 0$). However, in the case that if all other non-diagonal terms are zeros ($p^{ij} = 0$ for all $i \neq j$), it needs to impose on $p^{ii} = 1$. This treatment is made only for satisfying Eq.(4). It keeps the same meaning for a semi-Markov chain on the self-cycling times of its state.

Construction Rule 8: **Constraint to p^i_{mn}**. Transition of the microstates is restricted within the same macrostate but can be moved in two ways (normal or inverse normal directions).

Construction Rule 9: **Assumption for renewal process.** A binomial law is assumed as a result of Bernouilli observation for the renewal process [17]. Suppose x to be an integer variable for a class containing x items. The probability of the class having k items after N event steps is

$$P_r(x=k) = C^k_N b^k (1-b)^{N-k}, \tag{6}$$

where C^k_N is a binomial coefficient, and b is the probability of producing a new metamer or growth unit.

Construction Rule 10: **Assumption for death process.** Suppose c to be the probability of the bud surviving in each step. Then, the probability of a class, y, survived until (k-1) steps,

but in deadth at the kth step, is following a geometrical law as

$$P_d(y=k)=c^{k-1}(1-c). \tag{7}$$

Construction Rule 11: **Construction of data sets in database**. Specify parameters in respect to the groups, and put them into the corresponding sub-databases. For simplicity, we suggest to select as fewer parameters as possible, try to set them to be constant, and assume less coupling among the sub-databases. In GreenLab, we define a constant parameter set of database for topological plants by

$$\Omega_T = [(M^i), (m^i), (N^i), (n^i), (b^i), (c^i), (p^{ij}), (p^i{}_{mn})]. \tag{8}$$

An example is given in the next section by several tables. Note that a superscript is added onto b and c, but can be neglected if it is calculated within a known macrostate.

Theorem 1: **Compound probability for renewal-death process.** Suppose b and c are probabilities of forming a new metamer and of surviving the bud for a given macrostate, respectively. Within growth cycles possibly up to N, the compound probability of producing k growth units for the renewal-death process is given by:

$$P_c(x=k)=\sum_{j=k}^{N-1}(1-c)c^j C_j^k b^k (1-b)^{j-k} + c^N C_N^k b^k (1-b)^{N-k}. \tag{9}$$

Proof. Due to the probability of death in process, the number of growth cycles N may decrease. Consequently, Eq.(10) will give the probability consisting of several terms in accordance with the changing N:

$$\begin{aligned} P_c(x=k)=&(1-c)c^k C_k^k b^k (1-b)^{k-k} + (1-c)c^{k+1} C_{k+1}^k b^k (1-b)^{(k+1)-k} + \ldots \\ &(1-c)c^{N-1} C_{N-1}^k b^k (1-b)^{(N-1)-k} + c^N C_N^k b^k (1-b)^{N-k}. \end{aligned} \tag{10}$$

The first term on the right side of (9) indicates that the process goes to k cycles but terminates at the $(k+1)$th step. For this reason, the respective probability $C^k_k b^k (1-b)^{k-k}$ has to be multiplied by $(1-c)c^k$. All other terms follow the same rules for calculations. Combining all terms but the last one in Eq.(10), we obtain Eq.(9) for the compound probability in renewal-death process. Any process terminated before the $(k+1)$th step cannot produce k items.

Theorem 2: **Constraints for generating determined topological plants.** Since determined plants are assumed for ideal plants that undergo no stochastic process, we can attribute the constraints to the following probabilities:

$$b^i = c^i = 1, \text{ and } p^{ij} = p^i{}_{mn} = 1 \text{ (subject to Eq.(4))} \tag{11}$$

Proof. This theorem can be confirmed by observations. Firstly, when $b^i = c^i = 1$, it indicates that a new metamer or growth unit is always generated and survived in each step or growth cycle. Secondly, the next constraints for the transition matrixes enforce the determined transition from the current state into the specified state after its associated maximum self-cycling number is reached. Eq.(11) presents a complete set of constraints for generating determined topological plants.

5 Simulation Examples of Dual-Scale Automaton

The first example [23] is given to show a plant growth for a determined process. For realizing this, we set $b^i = c^i = 1$, and $p^{i(i+1)} = p^i{}_{m(m+1)} = 1$. In this example, a plant structure is divided into botanical units having three physiological ages. Fig.5(a) shows the dual-scale automaton for this plant.

According to the types of metamers shown in Table 2, we set five microstates, together with their geometrical data. Fig.5(b) illustrates the topological development of plant in respect to seven growth cycles.

All architectural models defined by botanists [15] are generated by the proposed dual-scale automaton [23]. The simulation results confirm the new approach to be a generic tool in modeling topological structures of plants.

In the second example [23], stochastic structures of plants are simulated. Using the same automaton in Fig.3(a) and geometrical data in Table 2, we apply the stochastic parameters from Table 3 to Table 5. Fig.6 presents three stands of stochastic plants. In each simulation, the structure changes and is different with a determined plant in Fig.5(e).

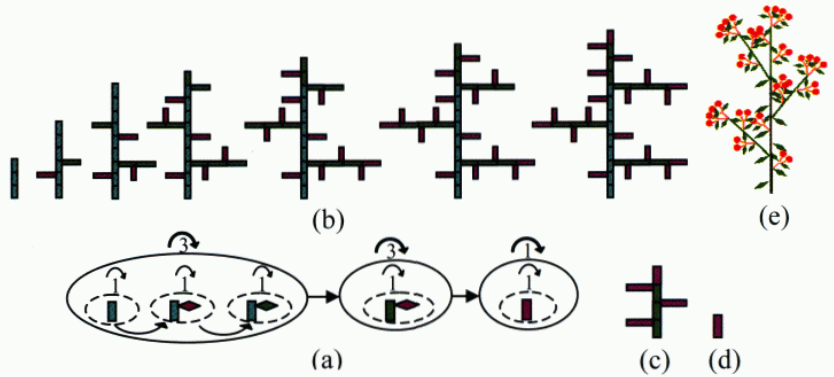

Fig.5 Dual-scale automaton for topological structures of a determined plant. (a) Automaton: dotted ellipse for microstate and solid one for macrostate. (b) Structures developing from 1st cycle to 7th cycle. The terminating structure is $S^7{}_1$. (c) Substructure $S^4{}_2$. (d) Substructure $S^1{}_3$. (e) 2D plant structure by integrating with geometrical parameters (after [23])

Table 2 Geometrical data for microstates [23]

Micro-state	*Axillary buds number*	*Leaves number*	*Flowers number*	*Axillary bud angle*	*Leaf angle*	*Flower angle*	*Corres-ponding metamer*
	0	1	0	0	120°	0	
	1	1	0	40°	120°	0	
	1	1	0	40°	120°	0	
	1	1	0	40°	120°	0	
	0	2	2	0	80°	20°	

Table 3 Parameters for renewal-death processes

Macrostate	*N*	*b*	*c*
M^1	3	0.6	0.95
M^2	3	0.5	0.0
M^3	1	0.0	0.0

Table 4 Transition matrix for macrostates

	M^1	M^2	M^3
M^1	0.0	0.9	0.1
M^2	0.0	0.0	1.0
M^3	0.0	0.0	1.0

Table 5 Transition matrix for the microstates inside the 1st macrostate

	m^1_1	m^1_2	m^1_3
m^1_1	0.0	0.9	0.1
m^1_2	0.2	0.0	0.8
m^1_3	0.5	0.5	0.0

Fig.6 Stochastic plants in comparison with its determined plant in Fig.5(e) (after [23])

6 Comparison and Discussions of Dual-Scale Automaton

In this section, we will make a comparison of dual-scale automaton with the L-system approach, since the later is often used in modeling of topological development of plant structures. In principle, an L-system is also an automaton, but extended its power by using rewriting grammars. In implementation, L-systems can be considered as a language-based approach. On the contrary, we define dual-scale automaton to be a graph-based approach. Although both approaches could be traced back from the same theoretical sources, and possibly equivalent in functionality of generating any plant structure, what the differences in implementation seems to be an immediate questions for users.

We will use the same example in Fig.5 to show the differences between two approaches. Following the design procedures in L-systems [1,4], we present the formal grammars, in Table 6, which generate the determined plant in Fig.5(e).

A total number of twelve productive rules, P_i, are used in the design of L-system. Although this design could be simplified by using fewer rules, one can immediately see the differences in implementation of both approaches. Several benefits are observed in using the dual-scale automaton approach.

I. Plant structures, in terms of metamers and growth units with the same physiological age, are explicitly modeled in respect to two scales, namely, microstate and macrostate, into the automaton. This strategy will help users to integrate their botanical knowledge to the designs of models.

II. Plant structures exhibit themselves in a format of graphical information. Formulating this kind of information by grammars is not an easy task even for a botanist. Nevertheless, a graph-based approach is readily preserving the best natural means to illustrate the spatial information. Therefore, this approach is much easier for users to understand and implement a structural model than using a language-based approach.

III. Although this new methodology developed specifically only for plant-structure-type modeling, it presents a generic tool with uniform procedures of design in regardless of any type of plant architectures. This means that the "Sequential-over-Hierarchical(**SoH**)"

structure of an automaton could be never changed to represent the temporal and spatial information of plants. Only parameters will be specified and adjusted in designs.

Table 6 Formal grammars of L-system in simulation of the plant structure in Fig.5(e)

ω:	$A_{0,0}$	Notes:
P_1:	$A_{i1,j1}$: (i1 < 1)&(j1 < 3) → $IA_{i1+1,j1}$	
P_2:	$A_{i1,j1}$: (i1 = 1)&(j1 < 3) → $B_{0,j1}$	A, B, C, D and E are five
P_3:	$B_{i2,j1}$: (i2 < 1)&(j1 < 3) → $I[E_{0,0}]B_{i2+1,j1}$	different microstates in Fig.5(b),
P_4:	$B_{i2,j1}$: (i2 = 1)&(j1 < 3) → $C_{0,j1}$	respectively.
P_5:	$C_{i3,j1}$: (i3 < 1)&(j1 < 3) → $I[D_{0,0}]C_{i3+1,j1}$	
P_6:	$C_{i3,j1}$: (i3 = 1)&(j1 < 2) → $A_{0,j1+1}$	I represents the generation of an
P_7:	$C_{i3,j1}$: (i3 = 1)&(j1 = 2) → $D_{0,0}$	internode.
P_8:	$D_{i4,j2}$: (i4 < 1)&(j2 < 3) → $I[E_{0,0}]D_{i4+1,j2}$	
P_9:	$D_{i4,j2}$: (i4 = 1)&(j2 < 2) → $D_{0,j2+1}$	i, j are unit counting indexes for
P_{10}:	$D_{i4,j2}$: (i4 = 1)&(j2 = 2) → $E_{0,0}$	microstates and macrostates,
P_{11}:	$E_{i5,j3}$: (i5 < 1)&(j3 < 3) → $IE_{i5+1,j3}$	respectively
P_{12}:	$E_{i5,j3}$: (i5 = 1)&(j3 < 2) → $E_{0,j3+1}$	

We recognize that the power of language-based approaches is missing in the dual-scale automaton approach. However, graphs in dual-scale automaton are possible to be transformed directly into a syntax format for a language or program communication.

7 Approach for Complex Plants or Forest

According to its simulation procedures, we can term dual-scale automaton to be a "bud-by-bud" approach. For forming a complete plant, this approach processes the microstate one by one in respect to event steps. Although this procedure is more similar to the form of a functioning bud bearing successively another bud for a real plant growth, the computational cost is quite expensive even for a complex plant, let alone for a forest.

In GreenLab, we propose a substructure modeling approach for building a complex plant structure and extend it even to a forest creation [24, 25]. Forest, as a typical natural scene, presents a great challenge in the studies of geometrical modeling and rendering. This is particularly true for applications in forestry. A proper model for forestry should be capable of not only generating all stands of trees, but also determining the yields of all trees in terms of each organ with a reasonable degree of accuracy. Therefore, apart from graphical resemblance consideration, this model has to be faithful to botanical principles.

In the proposed substructure approach, botanical knowledge is persistently followed in modeling stochastic structures of plants. The bases for applying substructures in modeling are given by [15, 26]:

- **Architectural model and unit**. Whatever degree of complexity, the growth pattern of plants can be described by a finite number of architectural models (twenty three in total [15]). For further classification of a specific species, an architectural unit is defined by including more information of morphological and functional characteristics. The idea of architectural model is so important that it simplifies the structural modeling of plants extremely. It lays down a solid botanical basis for

GreenLab to introduce a substructure strategy in modeling.

- **Baseline for modification**. Architectural models or units can be considered as a baseline representation. They form determined patterns of plants. The actual pattern of a real plant will result from "*an equilibrium between endogenous growth processes and the constraints exerted by the environment*"[26]. This knowledge suggests that a stochastic process should be imposed on the baselined architectural units, or substructures, for generating a real plant structure.
- **Reiteration**. A morphogenetic process through which the organism duplicates totally or partially its own elementary architectures. There exist several situations in this phenomenon. Reiteration property of plants strengthens requirements for the substructure strategy (or the similarity in Fractal modeling).

Now, we will present some definitions and construction rules for the stochastic substructure modeling in GreenLab.

Definition 1: **Substructures**. The term of substructure is a relative, with multi-level, description about the botanical units of plants. Any plant can be decomposed into a set of substructures. The smallest substructure is a single axis, which may have internode(s) from one to many. The biggest substructure is a whole plant itself. We can treat it in this way when modeling plants from the scale of forest or plantation. We define S^j_i to be a substructure with its bearing axis beginning from physiological age i and undergoing chronological age j. For the above two extreme cases of substructures, we use S^1_m for the smallest substructure having the oldest physiological age m. And, the final whole plant can be represented by S^n_1 as a substructure starting from physiological age 1, and terminating at chronological age n. Fig.5 shows three substructures for a determined plant.

Definition 2: **Substructure database**. Substructure database (or sub-database as termed in Eq.2) is built in GreenLab for a fast construction of a complex plant or forest. The sub-database is define by

$$\Omega_S = [(S^j_i)] \text{ for } j \in C = \{1, 2, \ldots, n\} \text{ and } i \in P = \{1, 2, \ldots, m\}, \qquad (12)$$

where n and m are the maximum chronological and physiological ages, respectively. In this definition, S^j_i becomes a data set including substructures defined by S^j_i. For this data set, we define $N(S^j_i)$ to be the sample size in association with substructure S^j_i.

Definition 3: **Topological yields of plants**. Yields are important production data in applications of agronomy and forestry. Three common types of yields can be defined in plant modeling and simulations, namely, topological, volume and weight. We define topological yield to be numbers of plant entities in respect to their entity types. The entity types could be a metamer, a growth unit, or a substructure. For metamer type, one can further define it into several classes in respect to the botanical organ types, like examples in Table 1 (see the right column in the Table). The yield data calculation within GreenLab model usually follows the order of "topological → weight → volume". Hence, topological yield is the fundamental data for calculation of other types of yield.

Construction Rule 1: **Selection of sample size of substructure database.** Two cases will be considered below.

Case 1: For a determined plant, the possible sample size of each substructure appears to be one. Then, we set

$$N(S^j_i) = N_t(S^j_i) = 1, \qquad (13)$$

where $N_t(S^j_i)$ is defined as the total number of possible sample(s) to the substructure S^j_i.

Case 2: When a stochastic process is introduced to a plant, the number of $N_t(S^j_i)$ will be

increased significantly. For a fast creation of a complex plant or forest, we set

$$0 \le N(S^j_i) < N_t(S^j_i) . \quad (14)$$

This indicates that we will use a smaller size of each substructure set with the same physiological and chronological ages to approximate an actual plant. Therefore, the selection of $N(S^j_i)$ in this case will be a "trial and error" procedure. Nevertheless, the heuristic knowledge exists. The bigger $N(S^j_i)$ in use, the better approximation in simulation.

Construction Rule 2: **Generation of substructures.** Based on a given data set of Ω_T, one can generate the resulting substructures by using the dual-scale automaton approach. All data will be arranged in a matrix format to form the database of Ω_S. This task, in fact, can be fulfilled as an off-line procedure.

Construction Rule 3: **Assembly of plant**. Rather than undergoing bud-by-bud procedures in generating a whole plat, this modeling approach will assemble a plant after retrievals of substructures from database of Ω_S. The assembly order will follow "top-down" directions, an inverse to the bud-by-bud, or "bottom-up", directions. If it is a stochastic structure of plant, the retrievals will be made by a random selection with a uniformly distribution on S^j_i.

The more detailed procedures for describing the substructure modeling approach can be referred to [24, 25]. While in [24] a determined plant is studied, a more general case of plants by including stochastic processes is investigated in [24]. The formulas for calculation of topological yield, as well as several examples, are given in their work.

8 Guideline of Generating Topological Plants in GreenLab

A guideline of generating topological plants is given in GreenLab. Both dual-scale automaton and substructure approaches are included in the framework. Among this, the former approach is a kernel, and is used always. The final output of this topological model in GreenLab is not only the graphical data for a specific plant, but also its topological yield. However, this set of data can be made through either one of two approaches, "bud-by-bud" (called A_b), or "substructure-by-substructure" (called A_s). Which approach should be adopted can be decided by either users or the selection module in the framework. This module provides an automatic selection of approaches based on a selection criterion defined by a cost ratio

$$r_c = \frac{\text{cost}(A_b)}{\text{cost}(A_s)} . \quad (15)$$

When this ratio is greater than a threshold (say, $r_c > 2$), a substructure approach will be adopted in modeling and simulation. While we have stated the benefits in using the dual-scale automaton approach, the advantages of applying the substructure approach will be summarized below.

I. This approach is able to integrate botanical knowledge of substructures, or architecture units, directly into modeling, which will simplify the modeling greatly.

II. Computational cost in plant creation is dramatically reduced in comparison with the conventional modeling (bud-by-bud) approach even for a complex plant [24, 25], let alone for a forest. It also provides a fast calculation of organ productions for plantation.

III. Due to its simplification from an early stage of modeling, the substructure approach preserves an efficient and promising solution to forest rendering, particularly in using a "level of detail (LoD)" technique.

As we see, the multilevel approach of plant architecture relies on synthetic notions from

metamers to substructures. This allows the modeling approach to concentrate more on the mathematical rules of production than in the formalism of the organs creation step by step. It leads to a very compact formalism that speeds up dramatically the plant construction.

9 Final remarks

In this presentation, we introduce a conceptual framework of GreenLab model. Only preliminary progresses in structural modeling are given. Other subjects under investigations include studies with functional parameters on some crops (e.g. wheat [27], sunflower, cotton, and tomato), biomass calculation and partition, stem and branch radial growth of a tree stand [25], and simulation of inflorescences [28]. We recognize that there is a long way for the model to provide reliable prediction power in applications to real systems. As a new methodology for functional-structural modeling of plant growth, GreenLab is facing challenges in many aspects [29]. In the course of further development of GreenLab model, the following three principles will be insisted:

I. Reliability. This is the most critical point for users to adopt a model in applications of agronomy and forestry.

II. Truthful to botanical knowledge. This principle will ensure the model to be true from its basis. Preserving the model with botanical meanings will be helpful for users to understand and to apply the model properly.

III. Simplicity. This principle should be pursued whenever it is possible. Simplicity of a model can be reflected by the following features: consistency and explicitness in mathematical expressions, parallelism and recursiveness in algorithms, parsimony and normalization in model parameters, high modularity and hierarchy in architectural organization, unification format in data flow, and graphical description for 3D information.

To emphasize the last principle, we cite quotations from great scientists about "simplicity" below, with a belief that their philosophy would guide a proper route in modeling a complex world.

"***God always acts in the simplest way***"**[30]**.

by Galileo Galilei (1564-1642)

"***Nature is pleased with simplicity and affects not the pomp of superfluous cause***" **[31]**.

by Isaac Newton (1642-1727)

"***Nature is the realization of the simplest conceivable mathematical ideas***" **[32]**.

by Albert Einstein (1879-1955)

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